

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 9, 2002, 16:22:02 ; Search time 45.81 Seconds
(without alignments)
1672.946 Million cell updates/sec

Title: US-09-880-887-9

Perfect score: 312
Sequence: 1 gttgtttatgcattctttt.....cgtattctttacatttcag 312

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA: *
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	312	100.0	312	US-09-526-935B-9	Sequence 9, Appl1
2	34.2	11.0	459	US-08-936-165A-23	Sequence 23, Appl1
3	33.2	10.6	19932	US-08-477-451-25	Sequence 25, Appl1
4	32.2	10.3	605	US-09-385-982-483	Sequence 483, Appl1
5	31.6	10.1	1564	US-08-904-234-2	Sequence 2, Appl1
6	31.6	10.1	2885	US-08-471-496-1	Sequence 1, Appl1
7	31.6	10.1	2885	US-08-894-840-1	Sequence 1, Appl1
8	31.6	10.1	2885	US-09-139-675-1	Sequence 1, Appl1
9	31.4	10.1	2022	US-08-505-486-96	Sequence 96, Appl1
10	31.4	10.1	2022	US-08-801-028-96	Sequence 96, Appl1
11	31.4	10.1	2022	US-09-340-154-96	Sequence 96, Appl1
12	31.4	10.1	2022	PCT-US95-09338-96	Sequence 96, Appl1
13	31.4	10.1	2022	PCT-US95-09339-96	Sequence 96, Appl1
14	31.4	10.1	2127	US-08-505-486-95	Sequence 96, Appl1
15	31.4	10.1	2127	US-08-801-028-95	Sequence 95, Appl1
16	31.4	10.1	2127	US-09-340-154-95	Sequence 95, Appl1
17	31.4	10.1	2127	PCT-US95-09338-95	Sequence 95, Appl1
18	31.4	10.1	2127	PCT-US95-09339-95	Sequence 95, Appl1
19	31.2	10.0	4517	US-09-140-804-9	Sequence 9, Appl1
20	31	9.9	81	US-08-232-463-44	Sequence 44, Appl1
21	31	9.9	2110	US-09-419-459-1	Sequence 1, Appl1
22	31	9.9	3943	US-08-369-796-3	Sequence 3, Appl1
23	31	9.9	3943	US-08-852-091-3	Sequence 3, Appl1
24	31	9.9	3943	US-08-820-754-3	Sequence 3, Appl1
25	31	9.9	3943	US-08-956-652-3	Sequence 3, Appl1
26	31	9.9	3943	US-08-956-869-3	Sequence 3, Appl1
27	31	9.9	3943	US-08-948-547-3	Sequence 3, Appl1

28	31	9.9	3943	US-09-364-970-10	Sequence 10, Appl1
29	31	9.9	3943	US-08-956-653A-3	Sequence 3, Appl1
30	31	9.9	3943	PCT-US95-17025-3	Sequence 3, Appl1
31	31	9.9	4003	US-09-087-465-1	Sequence 1, Appl1
32	31	9.9	9636	US-08-323-170B-1	Sequence 1, Appl1
33	31	9.9	9636	US-08-954-441-1	Sequence 1, Appl1
34	31	9.9	246240	US-08-724-394A-20	Sequence 20, Appl1
35	31	9.9	246240	US-08-724-394A-21	Sequence 21, Appl1
36	31	9.9	246240	US-08-724-394A-22	Sequence 22, Appl1
37	30.8	9.9	2099	US-08-299-849B-25	Sequence 25, Appl1
38	30.8	9.9	2099	US-08-142-368A-25	Sequence 25, Appl1
39	30.8	9.9	2099	US-08-967-727-25	Sequence 25, Appl1
40	30.8	9.9	2099	US-08-037-230D-25	Sequence 25, Appl1
41	30.8	9.9	2150	US-08-299-849B-24	Sequence 24, Appl1
42	30.8	9.9	2150	US-08-142-368A-24	Sequence 24, Appl1
43	30.8	9.9	2150	US-08-967-727-24	Sequence 24, Appl1
44	30.8	9.9	2150	US-08-037-230D-24	Sequence 24, Appl1
45	30.6	9.8	881	US-08-402-804-5	Sequence 5, Appl1

ALIGNMENTS

RESULT 1
US-09-526-935B-9
; Sequence 9, Application US/09526935B
; Patent No. 6271025
; GENERAL INFORMATION:
; APPLICANT: NEGRIER, CLAUDE
; APPLICANT: PLANTIER, JEAN LUC
; TITLE OF INVENTION: MODIFIED FACTOR VIII CDNA
; FILE REFERENCE: 06478.1441
; CURRENT APPLICATION NUMBER: US/09/526,935B
; CURRENT FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: EP 99104050.2
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 312
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-526-935B-9

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Best Local Similarity 100.0%; Pred. No. 4.9e-73;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	tatcatatcgtctcttcttcaactaaatttgattgattatgatacgaacattgaa	120
DB	61	tatcatatcgtctcttcttcaactaaatttgattgattatgatacgaacattgaa	120
QY	121	gtctaacagccagcagcggttggtgaagtaactgtggaacatcaacagatttgctca	180
DB	121	gtctaacagccagcagcggttggtgaagtaactgtggaacatcaacagatttgctca	180
QY	181	tgccccaagaagaatttgcttcaattatgattgataaacaagaacttctaaga	240
DB	181	tgccccaagaagaatttgcttcaattatgattgataaacaagaacttctaaga	240
QY	241	gatgtaaaatttcacatgatttctttttgctaaacaaagaattaacgcgtattct	300
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Oy 79 tcactaaatttgattacatgatgtgacagcataattgaagaqctcaacagccagcgc 138
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Db 2830 TCAGTTAAATTTTCTGTCTTCCTACCTTTATTCTCNAGAGCTCAAGAGGTTCAGTAN 2771

Query Match	10.1%;	Score 31.4;	DB 3;	Length 2022;
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[illegible]

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Db	431	TAGTTTATTCATGATTATTTAAGTAATAATTTGAATGTGTTTACATTATCAATATTAATTT	372	
QY	63	tcgatgctgcctccttcactaaatttgattacaagtgattgaacgaacataatt	115	
Db	371	AGTGACGGGTAAATTAATAAAAAAATTTGACCCTCTTGCTTATTAAGAATAATTT	319	

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1      RESULT 12
2      PCT-US95-09338-96/c
3      ; Sequence 96, Application PC/TUS9509338
4      ; GENERAL INFORMATION:
5      ; APPLICANT:
6      ; TITLE OF INVENTION:  UBIQUITIN-LYTIC PEPTIDE FUSION GENE
7      ; TITLE OF INVENTION:  CONSTRUCTS, PROTEIN PRODUCTS DERIVING THEREFROM, AND
8      ; TITLE OF INVENTION:  METHODS OF MAKING AND USING THE SAME
9      ; NUMBER OF SEQUENCES:  98
10     ; COMPUTER READABLE FORM:
11     ; MEDIUM TYPE:  Floppy disk
12     ; COMPUTER:  IBM PC compatible
13     ; OPERATING SYSTEM:  PC-DOS/MS-DOS
14     ; SOFTWARE:  WORDPERFECT 5.1+
15     ; CURRENT APPLICATION DATA:
16     ; APPLICATION NUMBER:  PCT/US95/09338
17     ; FILING DATE:  21-JUL-1994
18     ; PRIOR APPLICATION DATA:  08/279,472
19     ; APPLICATION NUMBER:  08/279,472
20     ; FILING DATE:  22-JUL-1994
21     ; INFORMATION FOR SEQ. ID NO:  96:
22     ; SEQUENCE CHARACTERISTICS:
23     ; LENGTH:  2022
24     ; TYPE:  NUCLEIC ACID
25     ; STRANDEDNESS:  DOUBLE STRANDED
26     ; TOPOLOGY:  LINEAR
27     ; MOLECULE TYPE:
28     ; DESCRIPTION:  GENOMIC DNA
29     ; PCT-US95-09338-96

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Query Match: 10.1%; Score 31.4; DB 5; Length 2022;
Best Local Similarity 54.9%; Pred No. 11;
Matches 62; Conservative 0; Mismatches 51; Indels 0; Gaps 0

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Db 431 TAGTGTATTCATGATGATTAAGTAAATTTGAATTGTTTACATATTCAAATTAATTT 372

Oy 63 tctatgctgtccttctcaactaaatttgatttaacttgttgaacgaataatt 115
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 371 AGTACGCTGATTAATTAATAAAAAAATTCACCTCTTGCTTTATAGAATAATTT 319

RESULT 13
PCT-US95-09339-96/C
Sequence 96, Application PC/TUS9509339
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: UBIQUITIN-LYRIC PEPTIDE FUSION GENE
TITLE OF INVENTION: CONSTRUCTS, PROTEIN PRODUCTS DERIVING THEREFROM, AND
TITLE OF INVENTION: METHODS OF MAKING AND USING THE SAME
NUMBER OF SEQUENCES: 98
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERECT 5.1+
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09339
FILING DATE: 21-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/279,472
FILING DATE: 22-JUL-1994
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 2022
TYPE: NUCLEIC ACID
STRANDEDNESS: DOUBLE STRANDED
TOPOLOGY: LINEAR
MOLECULE TYPE:

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Db 371 AGTGACGTGTATATATAAAAAATGACCTCTTGCTTATAAGAAATATT 319

Search completed: September 9, 2002, 21:17:29
Job time: 17727 sec